OPEN ACCESS Freely available online

ISSN: 2161-1041
Hereditary Genetics: Current Research

Short Communication

Genetic Variant Characteristics in ADME Genes Based on Whole-Exome Sequencing

Matthew Lammi*

Department of Genetics, University Stanford University, Stanford, United States of America

DESCRIPTION

The rapid evolution of genomic technologies has dramatically transformed the landscape of medical and pharmacogenomic research. Among the numerous approaches available, Whole-Exome Sequencing (WES) stands out as a powerful tool that enables comprehensive analysis of protein-coding regions of the genome. One of the most significant areas benefiting from WES is the study of genetic variants in ADME (Absorption, Distribution, Metabolism and Excretion) genes. These genes play an essential role in the pharmacokinetics of drugs, influencing their effectiveness and safety in individuals. This article delves into the importance of genetic variants in ADME genes, explores the impact of WES in identifying these variants and highlights the future implications of this research for personalized medicine [1-3].

ADME genes are responsible for encoding the enzymes, transporters and receptors that regulate the processes governing how drugs are absorbed, distributed, metabolized and excreted by the body. The functional diversity of these genes can lead to significant interindividual variability in drug response, which may result in therapeutic failure or adverse drug reactions. ADME-related genes include those encoding cytochrome P450 enzymes, drug transporters like ABC transporters and various receptors involved in drug signaling [4-6].

Enzymes in this family, such as CYP2D6, CYP3A4 and CYP1A2, are involved in the phase I metabolism of a wide range of pharmaceutical drugs. Variants in these genes can result in ultra-rapid, extensive, intermediate, or poor metabolism, affecting drug efficacy and toxicity.

These proteins regulate the absorption, distribution and elimination of drugs. Variants in these genes, such as *ABCB1*, can lead to differences in drug concentrations in the bloodstream and tissues, influencing drug action and side effects [7-9].

These enzymes are involved in the conjugation of drugs with endogenous molecules, facilitating their elimination. Variants in *UGT1A1*, for instance, are associated with altered metabolism of certain drugs, such as irinotecan.

The study of genetic variation within these genes is critical for understanding how genetic factors influence drug response and improving drug safety.

Whole-Exome Sequencing (WES) focuses on sequencing the protein-coding regions of the genome, which represent approximately 1% of the entire genome but harbor about 85% of disease-related variants. WES is an attractive method for identifying rare and common variants in ADME genes, offering a comprehensive approach to investigate the genetic underpinnings of drug response variability.

Unlike traditional candidate gene approaches, which focus on specific genes suspected of influencing drug response, WES allows for an unbiased, genome-wide search. This opens up new avenues for discovering novel variants, providing a deeper understanding of the genetic factors that contribute to pharmacokinetics. Moreover, WES enables researchers to identify both coding mutations and genetic variations that affect protein function, such as missense, nonsense and frameshift mutations.

The application of WES to ADME genes has already yielded important findings. For instance, rare variants in CYP genes and transporters have been associated with altered drug metabolism, leading to unexpected drug responses in patients. WES allows for the identification of both common and rare variants that may otherwise be overlooked by traditional genotyping methods [10].

CONCLUSION

Research on genetic variants in ADME genes, fueled by Whole-Exome Sequencing, is revolutionizing our understanding of drug metabolism and response. By identifying genetic variants that

Correspondence to: Matthew Lammi, Department of Genetics, University Stanford University, Stanford, United States of America, E-mail: lammimw@usyahoo.com

Received: 28-May-2024, Manuscript No. HGCR-24-28368; **Editor assigned:** 31-May-2024, PreQC No. HGCR-24-28368 (PQ); **Reviewed:** 14-Jun-2024, QC No. HGCR-24-28368; **Revised:** 21-Jun-2024, Manuscript No. HGCR-24-28368 (R); **Published:** 28-Jun-2024, DOI: 10.35248/2161-1041.24.13.286

Citation: Lammi M (2024). Genetic Variant Characteristics in ADME Genes Based on Whole-Exome Sequencing. Hereditary Genet. 13:286.

influence the absorption, distribution, metabolism and excretion of drugs, this research promises to enhance personalized medicine, optimize drug therapy and minimize adverse drug reactions. While challenges remain in terms of interpreting complex genetic data and ensuring its clinical utility, the future of pharmacogenomics looks promising. As sequencing technology becomes more advanced and affordable, the integration of genetic information into drug prescribing practices will likely become a cornerstone of precision medicine, ushering in an era of more effective, tailored treatments.

REFERENCES

1. González-Padilla D, Camara MD, Lauschke VM, Zhou Y. Population-scale variability of the human UDP-glycosyltransferase gene family. J Genet Genomics. 2024;51(11):1228-1236.
2. Tremmel R, Hu bschmann D, Schaeffeler E, Pirmann S, Frohling S, Schwab M. Innovation in cancer pharmacotherapy through integrative consideration of germline and tumor genomes. Pharmacol Rev. 2024;100014.
3. Gonzalez-Padilla D, Camara MD, Lauschke VM, Zhou Y. Population-scale variability of the human UDP-glycosyltransferase gene family. J Genet Genomics. 2024;51(11):1228-1236.
4. Santos M, Niemi M, Hiratsuka M, Kumondai M, Ingelman-Sundberg M, Lauschke VM, et al. Novel copy-number variations in pharmacogenes contribute to interindividual differences in drug pharmacokinetics. Genet Med. 2018;20(6):622-629.
5. Ingelman-Sundberg M, Lauschke VM. Individualized pharmacotherapy utilizing genetic biomarkers and novel in vitro systems as predictive tools for optimal drug development and treatment. Drug Metab Dispos. 2024;52(6):467-475.
6. da Silva IM, Vacario BG, Okuyama NC, Barcelos GR, Fuganti PE, Guembarovski RL, et al. Polymorphisms in drug-metabolizing genes and urinary bladder cancer susceptibility and prognosis: Possible impacts and future management. Gene. 2024;148252.
7. Jukic M, Milosavljevic F, Molden E, Ingelman-Sundberg M. Pharmacogenomics in treatment of depression and psychosis: An update. Trends Pharmacol Sci. 2022;43(12):1055-1069.
8. Cronin JM, Yu AM. Recombinant technologies facilitate drug metabolism, pharmacokinetics, and general biomedical research. Drug Metab Dispos. 2023;51(6):685-699.
9. Brion M, Quintela I, Sobrino B, Torres M, Allegue C, Carracedo A. New technologies in the genetic approach to sudden cardiac death in the young. Forensic Sci Int. 2010;203(1-3):15-24.
10. Trent RJ, Cheong PL, Chua EW, Kennedy MA. Progressing the utilisation of pharmacogenetics and pharmacogenomics into clinical care. Pathology. 2013;45(4):357-70.